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SEQUENCE LISTING

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<120> NOVEL SERINE PROTEASE BSSP5

<130> UEMURA=5

<140> 09/856,319

<141> 2001-05-21

<150> PCT/JP99/06473

<151> 1999-11-19

<150> JP 347806/1998

<151> 1998-11-20

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 1149

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (11)..(802)

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1 5 10

ggc tcc tcc tgg ggc tgc ggc att cct gcc atc aaa ccg gca ctg agc 97
Gly Ser Ser Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser
15 20 25

ttc agc cag agg att gtc aac ggg gag aat gca gtg ttg ggc tcc tgg 145
Phe Ser Gln Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp
30 35 40 45

ccc tgg cag gtg tcc ctg cag gac agc agc ggc ttc cac ttc tgc ggt 193
Pro Trp Gln Val Ser Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly
50 55 60

ggt tct ctc atc agc cag tcc tgg gtg gtc act gct gcc cac tgc aat 241
Gly Ser Leu Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn
65 70 75

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gtc agc cct ggc cgc cat ttt gtt gtc ctg ggc gag tat gac cga tca	289
Val Ser Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser	
80 85 90	
tca aac gca gag ccc ttg cag gtt ctg tcc gtc tct cgg gcc att aca	337
Ser Asn Ala Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr	
95 100 105	
cac cct agc tgg aac tct acc acc atg aac aat gac gtg acg ctg ctg	385
His Pro Ser Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu	
110 115 120 125	
aag ctc gcc tcg cca gcc cag tac aca aca cgc atc tcg cca gtt tgc	433
Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys	
130 135 140	
ctg gca tcc tca aac gag gct ctg act gaa ggc ctc acg tgt gtc acc	481
Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr	
145 150 155	
acc ggc tgg ggt cgc ctc agt ggc gtg ggc aat gtg aca cca gca cat	529
Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala His	
160 165 170	
ctg cag cag gtg gct ttg ccc ctg gtc act gtg aat cag tgc cgg cag	577
Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln	
175 180 185	
tac tgg gac tca agt atc act gac tcc atg atc tgt gca ggt ggc gca	625
Tyr Trp Asp Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala	
190 195 200 205	
ggt gcc tcc tcg tgc cag ggt gac tcc gga ggc cct ctt gtc tgc cag	673
Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln	
210 215 220	
aag gga aac aca tgg gtg ctt att ggt att gtc tcc tgg ggc acc aaa	721
Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys	
225 230 235	
aac tgc aat gtg cgc gca cct gct gtg tat act cga gtt agc aag ttc	769
Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe	
240 245 250	
agc acc tgg atc aac cag gtc ata gcc tac aac tgagctcacc acaggccctc	822
Ser Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn	
255 260	
cccagctcaa cccatttaaa ggacccaggc cctgtcccat catgcattca tgtctgtctt	882
cctggctcag gagaaagaag aggctgttga gggcccgact ccctacttgg acttctggca	942
cagaaggggc tgagtgactc cttgagtagc agtggctctt cctagagtag ccatgccgtg	1002
gccggggccc ccacccctcc tccagggcaa ccccttggtc ctacagcaag aagccagaac	1062
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 <211> 264
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 <213> Homo sapiens

<400> 2

Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu Gly Ser Ser
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Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln
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Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln
 35 40 45

Val Ser Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly Gly Ser Leu
 50 55 60

Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro
 65 70 75 80

Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala
 85 90 95

Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser
 100 105 110

Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu Lys Leu Ala
 115 120 125

Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys Leu Ala Ser
 130 135 140

Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr Thr Gly Trp
 145 150 155 160

Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala His Leu Gln Gln
 165 170 175

Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Asp
 180 185 190

Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala Gly Ala Ser
 195 200 205

09856319.052101

Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn
210 215 220

Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn
225 230 235 240

Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp
245 250 255

Ile Asn Gln Val Ile Ala Tyr Asn
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<211> 834
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ctt agc ctg gtc ctc ctt ggc tcc tcc tgg ggc tgt ggt gtt cct gcc 101
Leu Ser Leu Val Leu Leu Gly Ser Ser Trp Gly Cys Gly Val Pro Ala
10 15 20

atc acg cct gca ctg agc tac aat cag aga att gtc aac ggg gag aat 149
Ile Thr Pro Ala Leu Ser Tyr Asn Gln Arg Ile Val Asn Gly Glu Asn
25 30 35

gca gtg cca ggc tcc tgg ccc tgg cag gtg tct ctc cag gat aac acc 197
Ala Val Pro Gly Ser Trp Pro Trp Gln Val Ser Leu Gln Asp Asn Thr
40 45 50 55

ggc ttc cac ttc tgc ggt ggt tct ctc atc agt ccg aac tgg gtg gtc 245
Gly Phe His Phe Cys Gly Gly Ser Leu Ile Ser Pro Asn Trp Val Val
60 65 70

acg gct gcc cac tgc caa gtc acg cct gga cgc cac ttt gtc gtt ttg 293
Thr Ala Ala His Cys Gln Val Thr Pro Gly Arg His Phe Val Val Leu
75 80 85

gga gaa tat gac cga tct tcc aat gct gaa cct gtg cag gtc ctc tcg 341
Gly Glu Tyr Asp Arg Ser Ser Asn Ala Glu Pro Val Gln Val Leu Ser
90 95 100

atc gca agg gcc atc aca cac cct aac tgg aac gcc aac acc atg aac Ile Ala Arg Ala Ile Thr His Pro Asn Trp Asn Ala Asn Thr Met Asn 105 110 115	389
aat gac ctg act ctc ctg aag ctt gcc tcg cca gcc cgg tac aca gca Asn Asp Leu Thr Leu Leu Lys Leu Ala Ser Pro Ala Arg Tyr Thr Ala 120 125 130 135	437
caa gtc tca cca gtc tgc ctg gct tcc aca aac gag gca ctg cct tcg Gln Val Ser Pro Val Cys Leu Ala Ser Thr Asn Glu Ala Leu Pro Ser 140 145 150	485
ggg ctc acc tgt gtc acc act ggc tgg ggc cga atc agt ggt gtg ggc Gly Leu Thr Cys Val Thr Thr Gly Trp Gly Arg Ile Ser Gly Val Gly 155 160 165	533
aat gtg aca cca gct cgc ctg cag caa gtt gtt cta ccc ctg gtc act Asn Val Thr Pro Ala Arg Leu Gln Gln Val Val Leu Pro Leu Val Thr 170 175 180	581
gtg aat cag tgt cgg cag tac tgg ggt gca cgc att acc gat gcc atg Val Asn Gln Cys Arg Gln Tyr Trp Gly Ala Arg Ile Thr Asp Ala Met 185 190 195	629
ata tgt gca ggt ggc tca ggc gcc tcc tca tgt cag ggt gac tca gga Ile Cys Ala Gly Gly Ser Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly 200 205 210 215	677
ggc cct ctt gtc tgc cag aag gga aac acc tgg gtg ctt att ggg att Gly Pro Leu Val Cys Gln Lys Gly Asn Thr Trp Val Leu Ile Gly Ile 220 225 230	725
gtc tcc tgg ggc act aag aac tgc aac ata caa gca ccg gcc atg tac Val Ser Trp Gly Thr Lys Asn Cys Asn Ile Gln Ala Pro Ala Met Tyr 235 240 245	773
act cgg gtc agc aag ttc agt acc tgg atc aac caa gtc atg gcc tac Thr Arg Val Ser Lys Phe Ser Thr Trp Ile Asn Gln Val Met Ala Tyr 250 255 260	821
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<210> 4
<211> 264
<212> PRT
<213> mus sp.

<400> 4

Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu Gly Ser Ser
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Trp Gly Cys Gly Val Pro Ala Ile Thr Pro Ala Leu Ser Tyr Asn Gln
20 25 30

Arg Ile Val Asn Gly Glu Asn Ala Val Pro Gly Ser Trp Pro Trp Gln
35 40 45

Val Ser Leu Gln Asp Asn Thr Gly Phe His Phe Cys Gly Gly Ser Leu
50 55 60

Ile Ser Pro Asn Trp Val Val Thr Ala Ala His Cys Gln Val Thr Pro
65 70 75 80

Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala
85 90 95

Glu Pro Val Gln Val Leu Ser Ile Ala Arg Ala Ile Thr His Pro Asn
100 105 110

Trp Asn Ala Asn Thr Met Asn Asn Asp Leu Thr Leu Leu Lys Leu Ala
115 120 125

Ser Pro Ala Arg Tyr Thr Ala Gln Val Ser Pro Val Cys Leu Ala Ser
130 135 140

Thr Asn Glu Ala Leu Pro Ser Gly Leu Thr Cys Val Thr Thr Gly Trp
145 150 155 160

Gly Arg Ile Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln
165 170 175

Val Val Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly
180 185 190

Ala Arg Ile Thr Asp Ala Met Ile Cys Ala Gly Gly Ser Gly Ala Ser
195 200 205

Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn
210 215 220

Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn
225 230 235 240

Ile Gln Ala Pro Ala Met Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp
245 250 255

Ile Asn Gln Val Met Ala Tyr Asn
260

<210> 5
 <211> 99
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide to construct plasmid pSecTrypHis

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 tgctgcccc tttgacgacg atgacaagga tccgaattc 99

 <210> 6
 <211> 99
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide to construct plasmid pSecTrypHis

 <400> 6
 gaattcggat ccttgatcatc gtcgtcaaag ggggcagcaa cagcagcagc aacaaaggta 60
 aggatcagga gtagattcat ggtgttgcta gccaaagctt 99

 <210> 7
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to amplify neurosin-encoding
 sequence

 <400> 7
 ttggtgcatg gcgga 15

 <210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to amplify neurosin-encoding
 sequence

 <400> 8
 tcctcgagac ttggcctgaa tggtttt 27

 <210> 9
 <211> 35
 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pSecTrypHis/Neurosin

<400> 9
gcgctagcag atctccatga atctactcct gatcc 35

<210> 10
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pSecTrypHis/Neurosin

<400> 10
tgaagcttgc catggaccaa cttgtcatc 29

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pTrypHis

<400> 11
ccaagcttca ccatcaccat caccat 26

<210> 12
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pTrypSigTag

<400> 12
gcacagtcga ggctgat 17

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pFBTrypSigTag

<400> 13

caaatgtggt atggctg

17

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify conserved region of
serin proteases-encoding sequence

<220>
<221> misc_feature
<222> (9)..(9)
<223> "n" at position 9 is a, c, g or t

<220>
<221> misc_feature
<222> (12)..(12)
<223> "n" at position 12 is a, c, g or t

<400> 14
gtgctcacng cngcbcaytg

20

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify conserved region of
serin proteases-encoding sequence

<220>
<221> misc_feature
<222> (12)..(12)
<223> "n" at position 12 is a, c, g or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> "n" at position 15 is a, c, g or t

<400> 15
ccvctrwsdc cncnnggcga

20

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for RACE for hBSSP5 (forward)

<400> 16
tgtcagccct ggccgccatt 20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer for RACE for hBSSP5 (forward)

<400> 17
gcgagtatga ccgatcatca 20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer for RACE for hBSSP5 (reverse)

<400> 18
cgccacctgc acagatcatg 20

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer for RACE for hBSSP5 (reverse)

<400> 19
gaatcagtgc cggcagtact 20

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP5F1 to amplify full length hBSSP5 (forward)

<400> 20
tgccacgatg ttgctgctca 20

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer designated as hBSSP5F2 to amplify
 mature hBSSP5-encoding region (forward)

<400> 21
 attgtcaacg gggagaatgc 20

<210> 22
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer designated as hBSSP5R1/E to
 amplify full length hBSSP5 (reverse)

<400> 22
 ggaattcggg tctttaatgg gttgagc 27

<210> 23
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer designated as hBSSP5R4 for RT-PCR
 (reverse)

<400> 23
 cctggcacga ggaggcac 18

<210> 24
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer designated as mBSSP5F1 for RACE
 for mBSSP5 (forward)

<400> 24
 accatgaaca atgacctgac 20

<210> 25
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer designated as mBSSP5F2 for RACE
 for mBSSP5 (forward)

<400> 25
 gaatcagtgt cggcagt 17

<210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as mBSSP5F3 to amplify
 full length mBSSP5 (forward)

 <400> 26
 gaccatctca acaccattcc 20

 <210> 27
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as mBSSP5Fmature to
 amplify mature mBSSP5-encoding region (forward)

 <400> 27
 attgtcaacg gggagaatgc 20

 <210> 28
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as mBSSP5.1 for RACE
 for mBSSP5 (reverse)

 <400> 28
 atggcatcgg taatgcgtgc 20

 <210> 29
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as mBSSP5R2 for RACE
 for mBSSP5 (reverse)

 <400> 29
 caggtgtttc ctttctggca 20

 <210> 30
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5R3/E to amplify full length mBSSP5 (reverse)

<400> 30

ggaattcgga cagtttagtt gtaggcc

27

<210> 31

<211> 117

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 31

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tgctgcccc tttcaccatc accatcacca tgacgacgat gacaaggatc cgaattc 117

<210> 32

<211> 117

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 32

gaattcggat ccttgatcgc gtcgtcatgg tgatggtgat ggtgaaaggg ggcagcaaca 60

gcagcagcaa caaaggtaag gatcaggagt agattcatgg tgttgctagc caagctt 117

<210> 33

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 33

Asp Asp Asp Asp Lys

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5